

SEQUENCE LISTING

<110> Abrahmsén , Lars
Nilsson, Joakim

<120> METHODS FOR PROTEIN PURIFICATION

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<151> 2001-02-23

<150> US 60/272,247

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Cys Val Leu Leu Val Gly Arg Gly Gly Asp Gly Gly Glu Pro Ser Gln	
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Gln Pro Trp Thr His Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser
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Arg Glu Glu Leu Thr Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly
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Pro Gly Leu Val Asp Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val
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Phe Ser Val Glu Leu Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His
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Leu Asp Arg Gly Ser Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val
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Phe Phe Gly Arg Gln Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly
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Gly Gly Pro Leu Pro Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr
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 Thr Trp Phe Gly Leu Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu
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 His His Val Gly Leu Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro
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 Ala Arg Trp Thr Ile Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp
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 Pro Val Pro Pro Gly Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly
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 325 330 335
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 Val Asp Gly Gly Phe Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg
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 Gly Val Asp Cys Pro Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu
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15

20

25

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35

40

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45

50

55

60

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Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala

65

70

75

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80

85

90

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Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg

95

100

105

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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
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Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		

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Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
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Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
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<211> 218

<212> PRT

<213> Schistosoma japonicum

<400> 5

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Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
	50					55					60						
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
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Met	Leu	Gly	Gly	Ser	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
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Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
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Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
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Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Ser	His	Lys	Thr	Tyr	Leu	Asn		
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
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Val	Ser	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
		180					185						190				
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
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Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys								
	210					215											

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<213> Artificial Sequence

<220>

<223> Protease cleavage site

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43

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36

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21

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37

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<212> DNA

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48

atc aac gcc gcg caa cac gat gaa gcc gta gac aac aaa ttc aac aaa
Ile Asn Ala Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
20 25 30

96

gaa caa caa aac gcg tcc cct ata cta ggt tat tgg aaa att aag ggc
Glu Gln Gln Asn Ala Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly
35 40 45

144

ctt gtg caa ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat
Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
50 55 60

192

gaa gag cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa
Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
65 70 75 80

240

aag ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat
Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
85 90 95

288

ggt gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata gct
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
100 105 110

336

gac aag cac aac atg ttg ggt ggt tct cca aaa gag cgc gca gag att

384

Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Ser	Pro	Lys	Glu	Arg	Ala	Glu	Ile	
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Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	
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Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	
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Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Ser	His	Lys	
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aca	tat	tta	aat	ggg	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	576
Thr	Tyr	Leu	Asn	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	
			180					185					190			
gac	gct	ctt	gat	gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	624
Asp	Ala	Leu	Asp	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	
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Phe	Pro	Lys	Leu	Val	Ser	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	
	210						215				220					
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Gly	Trp	Gln	Ala	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Gln	
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Ser	Gln	Glu	Ala	Leu	Phe	Gln	Gly	Gly	Asp	Gly	Gly	Glu	Pro	Ser	Gln	
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Leu	Pro	His	Cys	Pro	Ser	Val	Ser	Pro	Ser	Ala	Gln	Pro	Trp	Thr	His	
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cct	ggc	cag	agc	cag	ctg	ttt	gca	gac	ctg	agc	cga	gag	gag	ctg	acg	912
Pro	Gly	Gln	Ser	Gln	Leu	Phe	Ala	Asp	Leu	Ser	Arg	Glu	Glu	Leu	Thr	
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Ala	Ala	Gln	Ala	Arg	Pro	Ser	Asp	Asn	Cys	Val	Phe	Ser	Val	Glu	Leu	
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cag	ctg	cct	ccc	aag	gct	gca	gcc	ctg	gct	cac	ttg	gac	agg	ggg	agc	1056
Gln	Leu	Pro	Pro	Lys	Ala	Ala	Ala	Leu	Ala	His	Leu	Asp	Arg	Gly	Ser	

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ccc Pro	cca Pro	cct Pro	gcc Ala	cgg Arg	gag Glu	gca Ala	ctg Leu	gcc Ala	atc Ile	gtc Val	ttc Phe	ttt Phe	ggc Gly	agg Arg	caa Gln	1104
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370					375					380						
tcc Ser	tac Tyr	atg Met	cgg Arg	gac Asp	gtg Val	act Thr	gtg Val	gag Glu	cgt Arg	cat His	gga Gly	ggc Gly	ccc Pro	ctg Leu	ccc Pro	1200
385					390					395					400	
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405					410					415						
atg Met	atc Ile	ttc Phe	aac Asn	aga Arg	gag Glu	ctg Leu	ccc Pro	cag Gln	gct Ala	tct Ser	ggg Gly	ctt Leu	ctc Leu	cac His	cac His	1296
420					425					430						
tgt Cys	tgc Cys	ttc Phe	tac Tyr	aag Lys	cac His	cgg Arg	gga Gly	cgg Arg	aac Asn	ctg Leu	gtg Val	aca Thr	atg Met	acc Thr	acg Thr	1344
435					440					445						
gct Ala	ccc Pro	cgt Arg	ggt Gly	ctg Leu	caa Gln	tca Ser	ggg Gly	gac Asp	cgg Arg	gcc Ala	acc Thr	tgg Trp	ttt Phe	ggc Gly	ctc Leu	1392
450					455					460						
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485					490					495						
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Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu	
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aga cta gtt tat gag ata agc ctc caa gag gcc ttg gcc atc tat ggt	1824
Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly	
595 600 605	
gga aat tcc cca gca gca atg acg acc cgc tat gtg gat gga ggc ttt	1872
Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe	
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Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro	
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Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala	
645 650 655	
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Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly	
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ctc ccc ctg cgg cga cac cac tca gat ctc tac tcg cac tac ttt ggg	2064
Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly	
675 680 685	
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690 695 700	
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Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile	
705 710 715 720	
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Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe	
725 730 735	
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Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly	
740 745 750	
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Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala	
755 760 765	
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Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met	
770 775 780	
gct gtg ccc tgg agc cct gag cac cag ctg cag agg ctg cag gtg acc	2400
Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr	
785 790 795 800	

cgg aag ctg ctg gag atg gag gag cag gcc gcc ttc ctc gtg gga agc	2448
Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser	
805 810 815	
gcc acc cct cgc tac ctg tac ctg gcc agc aac cac agc aac aag tgg	2496
Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp	
820 825 830	
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Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu	
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Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg	
850 855 860	
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Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser	
865 870 875 880	
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Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser	
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Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn	
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Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe	
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Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys	
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      35           40           45
Leu Val Gln Pro Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr
      50           55           60
Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys
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Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
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Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala
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Asp Lys His Asn Met Leu Gly Gly Ser Pro Lys Glu Arg Ala Glu Ile
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Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
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Ser Gln Glu Ala Leu Phe Gln Gly Gly Asp Gly Gly Glu Pro Ser Gln
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Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His
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Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr
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Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His Leu Asp Arg Gly Ser
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Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val Phe Phe Gly Arg Gln
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Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln
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 Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
 675 680 685
 Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
 690 695 700
 Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
 705 710 715 720
 Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
 725 730 735
 Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
 740 745 750
 Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
 755 760 765
 Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
 770 775 780
 Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
 785 790 795 800
 Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
 805 810 815
 Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
 820 825 830
 Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
 835 840 845
 Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg
 850 855 860
 Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser

